

## DISEASE NOTE

**FIRST REPORT OF *PHYTOPHTHORA NICOTIANAE* ON *CATHARANTHUS ROSEUS* IN BANGLADESH**T. Farhana<sup>1</sup>, R.L. Wick<sup>2</sup> and M.T. Islam<sup>1</sup><sup>1</sup>Department of Biotechnology, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh<sup>2</sup>Stockbridge School of Agriculture, University of Massachusetts, Amherst MA 01003, USA

Annual vinca (*Catharanthus roseus*), also known as Madagascar periwinkle, is native to the island of Madagascar, and now common in many tropical and subtropical regions worldwide, including Bangladesh (Chevallier, 1996). It has long been cultivated for herbal medicine and as an ornamental plant. Symptoms of stem canker and leaf blight developed on *C. roseus* in a landscape planting at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh, in June, 2014. To identify the pathogen, infected leaves were placed in water for 48 h, then the mycelia were transferred onto corn meal agar plates. Mycelial growth was patchy and irregular, coenocytic and tufted with an arachnoid branching habit, consistent with descriptions of *Phytophthora nicotianae*. The pathogen was also cultured on PARP medium (Ferguson and Jeffers, 1999) and V8 agar medium and pure cultures were established. Mycelial blocks (6 mm in diameter) were placed in sterile water for 3 days, then at 5°C for 15 min in the dark to stimulate production of sporangia and zoospores. Molecular identification was done by amplifying the ITS region of nuclear rDNA using ITS 4 and ITS 6 primer pairs. BLAST search revealed that the isolate had 100% identity with *P. nicotianae* (GenBank accession No. KT175508.1). The nucleotide sequence was deposited in GenBank under accession No. KU244700. Pathogenicity tests were conducted by inoculating *Catharanthus* leaves, previously wounded by pricking with a sterile needle, with 50 µl and 100 µl aliquots of zoospores. Foliar symptoms consistent with blight observed in the field developed on all the inoculated leaves after 72 h. Koch's postulates were fulfilled by re-isolating the pathogen from the lesions on the inoculated leaves. To our knowledge, this is the first molecular identification of *P. nicotianae* on *Catharanthus* in Bangladesh.

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**FIRST REPORT OF *CUCUMBER MOSAIC VIRUS* INFECTING APPLE IN CHINA**Y. Hu<sup>1</sup>, H.W. Shi<sup>1</sup>, C.C. Jing<sup>1</sup>, K. Li<sup>1</sup>, X.C. Sun<sup>1</sup>, G.T. Wu<sup>1</sup>, C.Y. Zhou<sup>2</sup> and L. Qing<sup>1,2</sup><sup>1</sup>Chongqing Key Laboratory of Plant Disease Biology, College of Plant Protection, Southwest University, Chongqing, 400716, P.R. China<sup>2</sup>Citrus Research Institute, Chinese Academy of Agricultural Sciences, Chongqing, 400712, P.R. China

A survey for apple viruses was conducted in October of 2014 in Shanxi, Gansu, Sichuan, Liaoning and Hebei provinces of China. A total of 189 leaf samples with mosaic symptoms and five symptomless samples were collected and tested for viruses. *Apple mosaic virus* (ApMV) (Lakshmi *et al.*, 2011; Robertson, 2012) was not detected by RT-PCR with total RNA and primers ApMV-F (5'-CGTGAGGAAGTTTAGGTTG-3')/ApMV-R (5'-GCCTCCTAATCGGGGCATCAA-3'). Neither were *Tobacco mosaic virus* (TMV), *Turnip mosaic virus* (TuMV), *Potato virus Y* (PVY) and *Potato virus X* (PVX) by a multiplex RT-PCR assay previously developed in our laboratory, with the exception of *Cucumber mosaic virus* (CMV), for which a partial fragment (322 bp) of the coat protein (CP) gene was amplified from 153 symptomatic samples using specific primers CMV-F (5'-GATAAGAAGCTTGTTTCGCG-3')/CMV-R (5'-GCTCGATGTCGACATGAAGT-3'). To confirm these preliminary results, primer pair CMV-CP-F (5'-ATGGACAAATCTGAATCAACC-3')/CMV-CP-R (5'-TCAGACTGGGAGCACCCC-3') were designed to amplify a 657 bp CMV CP amplicon by simplex RT-PCR. The expected product was obtained from each sample identified as positive by multiplex RT-PCR. Five amplicons were randomly selected for cloning and sequencing (GenBank accession Nos. KP307919-KP307922 and KP641344). Sequence alignments showed the highest CMV sequence identity at the nucleotide level (97.3% to 99.2%) of the five isolates with that of a CMV isolate from tobacco in Sichuan province (KJ746016). Phylogenetic analysis indicated the five isolates cluster into CMV subgroup I. Using the CMV-specific monoclonal antibody 3C12 (Yu *et al.*, 2005), the 153 symptomatic samples were positive for CMV in ELISA. No virus was detected in the five symptomless samples. To our knowledge, this is the first report of CMV infecting apple in China.

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